

# SEQUENCE LISTING

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<120> GEMINIVIRUS RESISTANT TRANSGENIC PLANTS

<130> 5051.458IP

<150> US 09/289,346

<151> 1999-04-09

<150> US 60/125,004

<151> 1999-03-18

<160> 112

<170> PatentIn version 3.2

<210> 1

<211> 352

<212> PRT

<213> Tomato golden mosaic virus

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Leu	Gln	Ala	Leu	Asn	Thr	Pro	Ile	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys
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Arg	Glu	Leu	His	Glu	Asp	Gly	Gln	Pro	His	Leu	His	Val	Leu	Ile	Gln
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Phe	Glu	Gly	Lys	Tyr	Cys	Cys	Gln	Asn	Gln	Arg	Phe	Phe	Asp	Leu	Val
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Ser	Pro	Thr	Arg	Ser	Ala	His	Phe	His	Pro	Asn	Ile	Gln	Arg	Ala	Lys
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Ser	Ser	Ser	Asp	Val	Lys	Thr	Tyr	Ile	Asp	Lys	Asp	Gly	Asp	Thr	Leu
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Val	Trp	Gly	Glu	Phe	Gln	Val	Asp	Gly	Arg	Ser	Ala	Arg	Gly	Gly	Cys
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Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys  
 130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser  
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp  
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn  
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys  
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu  
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn  
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile  
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
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Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
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Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
 35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe  
 50 55 60

Asp Lys Thr Pro Glu Pro  
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser  
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Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
 35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe  
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Asp Lys Thr Pro Glu Pro  
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<223> E--N140 + KEE146 (Ala4+5) mutation

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Ser Ala Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
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Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe  
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Asp Lys Thr Pro Glu Pro  
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 <223> Q-HN165 (Ala8) mutation

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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser  
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Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
 35 40 45

Tyr Leu Phe Ala Phe Ala Ala Leu Asn Ser Asn Leu Asp Arg Ile Phe  
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Asp Lys Thr Pro Glu Pro  
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser  
 20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
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Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Ala Leu Ala Ala Ile Phe  
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Asp Lys Thr Pro Glu Pro  
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1 5 10 15

Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser  
20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
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Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe  
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Asp Lys Thr Pro Glu Pro  
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser  
20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
 35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe  
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Asp Lys Thr Pro Glu Pro  
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Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
 35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe  
 50 55 60

Asp Lys Thr Pro Glu Pro  
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Gly Cys Ala Ala Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser  
20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe  
50 55 60

Asp Lys Thr Pro Glu Pro  
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Gly Cys Gln Thr Ser Ala Ala Ala Ala Ala Glu Ala Leu Asn Ala Ser  
20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe  
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Asp Lys Thr Pro Glu Pro  
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Ala Ala Leu Ala Ala Ser  
20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe  
50 55 60

Asp Lys Thr Pro Glu Pro  
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser  
20 25 30

Ser Ala Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe

50

55

60

Asp Lys Thr Pro Glu Pro  
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Glu Ala Leu Asn Ala Ser  
20 25 30

Ser Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe  
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Asp Ala Thr Pro Ala Pro  
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser  
 20 25 30

Ser Ala Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
 35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe  
 50 55 60

Asp Lys Thr Pro Glu Pro  
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser  
 20 25 30

Ser Lys Ala Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
 35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe  
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Asp Lys Thr Pro Glu Pro  
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20 25 30

Ser Lys Glu Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe  
50 55 60

Asp Lys Thr Pro Glu Pro  
65 70

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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser  
20 25 30

Ser Lys Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe  
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Asp Lys Thr Pro Glu Pro  
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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser  
 20 25 30

Ser Lys Glu Glu Tyr Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
 35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe  
 50 55 60

Asp Lys Thr Pro Glu Pro  
 65 70

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 <223> L148 mutation

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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser  
 20 25 30

Ser Lys Glu Glu Ala Ala Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
 35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe  
50 55 60

Asp Lys Thr Pro Glu Pro  
65 70

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Gly Cys Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser  
20 25 30

Ser Lys Glu Glu Ala Val Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
35 40 45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe  
50 55 60

Asp Lys Thr Pro Glu Pro  
65 70

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                     20                      25                      30  
 Ser Lys Glu Glu Ala Gly Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys  
                     35                      40                      45  
 Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe  
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 Asp Lys Thr Pro Glu Pro  
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                     20                      25                      30

Ser Lys Glu Glu Ala Leu Gln Ala Ala Arg Glu Lys Ile Pro Glu Lys  
                     35                      40                      45

Tyr Leu Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe  
                     50                      55                      60

Asp Lys Thr Pro Glu Pro  
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 atcaaataac gcagctagcg cgctatttag attgtg 36  
  
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 gaagccatgg cgccggagtc gcatcaaata tcc 33  
  
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 <223> TGMV AL1 coding sequence

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cagtgtctct tgtccaaaga agaatcactt tctcaattac aagccctaaa cactccgatt      120

aacaaaaaat tcataaaaat ctgcagagag cttcatgaag atgggcaacc tcacctccac      180

gtgcttattc agttcgaggg aaaatactgc tgccaaaatc aacgattctt cgacctggta      240

tccccacaaa ggtcagcaca tttccatcca aacattcaga gagctaaatc gtcttccgac      300

gtcaagacgt acatcgacaa agacggagat actcttgtat ggggagaatt ccaggtcgac      360

ggtcgaagtg ctagaggagg ttgccaaaca tctaacgacg ctgcagcaga ggcgttaaatt      420

gcttcttcca aagaagaagc cctgcagata attagagaga aaatcccaga aaaatattta      480

tttcagttcc acaatctaaa tagcaattta gataggatat ttgataagac tcctgaacca      540

tggttctctc cgttccacgt ctcatcattt actaacgtgc cagacgagat gagacaatgg      600

gctgaaaatt attttgaaa gagttccgct gcgcggccgg agagacctat tagtattatc      660

atcgagggcg atagtcggac gggaaagact atgtgggctc gttcactagg cccacataat      720

tatttgagcg ggcatttgga tctcaattct agggtttact caaacaaggt tgagtataac      780

gtcatcgatg atgtcacacc gcaatatcta aagttgaaac attggaaaga actcattggg      840

gccc aaagag attggcagac taactgtaaa tacggaaagc cagttcaaatt taaaggaggt      900

atcccgctcaa tcgtgctgtg caatcctgga gaggggtgcta gctataaagt tttcctcgac      960

aaagaggaaa aactccact aaagaactgg actttccata atgcgaaatt cgtcttctct 1020

aactcccccc tctatcaaag ctcaacacag agcagc                                1056
  
```

<210> 51  
 <211> 1056  
 <212> DNA  
 <213> Tomato golden mosaic virus

<220>  
 <221> CDS  
 <222> (1)..(1056)  
 <223> TGMV AL1 FQ118 mutant (Ala13)

<400> 51

atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt	48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe	
1 5 10 15	
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa	96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	
20 25 30	
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc	144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	
35 40 45	
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag	192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	
50 55 60	
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta	240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	
65 70 75 80	
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	
gta tgg gga gaa gcc gcg gtc gac ggt cga agt gct aga gga ggt tgc	384
Val Trp Gly Glu Ala Ala Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	
115 120 125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa	432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	
130 135 140	
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta	480
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	
145 150 155 160	
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	

agc cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 52  
 <211> 352  
 <212> PRT  
 <213> Tomato golden mosaic virus

<400> 52

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe	
1 5 10 15	
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	
20 25 30	
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	
35 40 45	
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	
50 55 60	



Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
100 105 110

Val Trp Gly Glu Ala Ala Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys  
130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser  
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp  
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn  
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys  
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu  
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn  
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile

290		295		300
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp				
305		310	315	320
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys				
	325		330	335
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser				
	340	345		350

<210> 53  
 <211> 1056  
 <212> DNA  
 <213> Tomato golden mosaic virus

<220>  
 <221> CDS  
 <222> (1)..(1056)  
 <223> TGMV AL1 D120 (Ala14) mutant

<400> 53	
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt	48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe	
1 5 10 15	
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa	96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	
20 25 30	
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc	144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	
35 40 45	
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag	192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	
50 55 60	
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta	240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	
65 70 75 80	
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	
gta tgg gga gaa gcc gcg gtc gcc ggc cga agt gct aga gga ggt tgc	384
Val Trp Gly Glu Ala Ala Val Ala Gly Arg Ser Ala Arg Gly Gly Cys	

115	120	125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys 130 135 140			432
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu 145 150 155 160			480
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys 165 170 175			528
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn 180 185 190			576
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser 195 200 205			624
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp 210 215 220			672
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn 225 230 235 240			720
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys 245 250 255			768
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu 260 265 270			816
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn 275 280 285			864
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile 290 295 300			912
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp 305 310 315 320			960
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys 325 330 335			1008
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser 340 345 350			1056

<210> 54  
 <211> 352  
 <212> PRT  
 <213> Tomato golden mosaic virus

<400> 54

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
 1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
 20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
 35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
 50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
 65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
 100 105 110

Val Trp Gly Glu Ala Ala Val Ala Gly Arg Ser Ala Arg Gly Gly Cys  
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys  
 130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser  
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp  
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn  
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys  
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu  
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn  
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile  
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
 340 345 350

<210> 55  
 <211> 1056  
 <212> DNA  
 <213> Tomato golden mosaic virus

<220>  
 <221> CDS  
 <222> (1)..(1056)  
 <223> TGMV AL1 RS-R125 (Ala1) mutant

<400> 55  
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48  
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
 1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	
20 25 30	
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc	144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	
35 40 45	
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag	192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	
50 55 60	
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta	240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	
65 70 75 80	
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	
gta tgg gga gaa ttc cag gtc gac ggt gcg gcc gct gca gga ggt tgc	384
Val Trp Gly Glu Phe Gln Val Asp Gly Ala Ala Ala Gly Gly Cys	
115 120 125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa	432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	
130 135 140	
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta	480
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	
145 150 155 160	
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	

	245	250	255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg				816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu				
	260	265	270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac				864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn				
	275	280	285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc				912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile				
	290	295	300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac				960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp				
	305	310	315	320
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa				1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys				
	325	330	335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc				1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser				
	340	345	350	

<210> 56  
 <211> 352  
 <212> PRT  
 <213> Tomato golden mosaic virus

<400> 56

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe			
1	5	10	15
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln			
	20	25	30
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys			
	35	40	45
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln			
	50	55	60
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val			
	65	70	75
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys			
	85	90	95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Ala Ala Ala Ala Gly Gly Cys  
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys  
 130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser  
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp  
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn  
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys  
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu  
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn  
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile  
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
 305 310 315 320



Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
 340 345 350

<210> 57  
 <211> 1056  
 <212> DNA  
 <213> Tomato golden mosaic virus

<220>  
 <221> CDS  
 <222> (1)..(1056)  
 <223> TGMV AL1 QT130 (Ala2) mutant

<400> 57  
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48  
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
 1 5 10 15  
 ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96  
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
 20 25 30  
 tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144  
 Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
 35 40 45  
 aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192  
 Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
 50 55 60  
 ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240  
 Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
 65 70 75 80  
 tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288  
 Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
 85 90 95  
 tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336  
 Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
 100 105 110  
 gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384  
 Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
 115 120 125  
 gca gct agc aac gac gct gca gca gag gcg tta aat gct tct tcc aaa 432  
 Ala Ala Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys  
 130 135 140  
 gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta 480

Glu	Glu	Ala	Leu	Gln	Ile	Ile	Arg	Glu	Lys	Ile	Pro	Glu	Lys	Tyr	Leu	
145					150					155					160	
ttt	cag	ttc	cac	aat	cta	aat	agc	aat	tta	gat	agg	ata	ttt	gat	aag	528
Phe	Gln	Phe	His	Asn	Leu	Asn	Ser	Asn	Leu	Asp	Arg	Ile	Phe	Asp	Lys	
				165					170					175		
act	cct	gaa	cca	tgg	ctt	cct	ccg	ttc	cac	gtc	tca	tca	ttt	act	aac	576
Thr	Pro	Glu	Pro	Trp	Leu	Pro	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn	
			180					185					190			
gtg	cca	gac	gag	atg	aga	caa	tgg	gct	gaa	aat	tat	ttt	gga	aag	agt	624
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr	Phe	Gly	Lys	Ser	
		195					200					205				
tcc	gct	gcg	cgg	ccg	gag	aga	cct	att	agt	att	atc	atc	gag	ggc	gat	672
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Ile	Glu	Gly	Asp	
	210					215					220					
agt	cgg	acg	gga	aag	act	atg	tgg	gct	cgt	tca	cta	ggc	cca	cat	aat	720
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn	
225					230				235						240	
tat	ttg	agc	ggg	cat	ttg	gat	ctc	aat	tct	agg	gtt	tac	tca	aac	aag	768
Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys	
				245				250						255		
gtt	gag	tat	aac	gtc	atc	gat	gat	gtc	aca	ccg	caa	tat	cta	aag	ttg	816
Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu	
			260					265					270			
aaa	cat	tgg	aaa	gaa	ctc	att	ggg	gcc	caa	aga	gat	tgg	cag	act	aac	864
Lys	His	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn	
		275					280					285				
tgt	aaa	tac	gga	aag	cca	gtt	caa	att	aaa	gga	ggg	atc	ccg	tca	atc	912
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile	
	290					295					300					
gtg	ctg	tgc	aat	cct	gga	gag	ggg	gct	agc	tat	aaa	gtt	ttc	ctc	gac	960
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp	
305				310					315					320		
aaa	gag	gaa	aac	act	cca	cta	aag	aac	tgg	act	ttc	cat	aat	gcg	aaa	1008
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys	
				325				330						335		
ttc	gtc	ttc	ctc	aac	tcc	ccc	ctc	tat	caa	agc	tca	aca	cag	agc	agc	1056
Phe	Val	Phe	Leu	Asn	Ser	Pro	Leu	Tyr	Gln	Ser	Ser	Thr	Gln	Ser	Ser	
			340				345						350			

<210> 58  
 <211> 352  
 <212> PRT  
 <213> Tomato golden mosaic virus

<400> 58

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
115 120 125

Ala Ala Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys  
130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser  
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp  
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn  
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys  
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu  
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn  
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile  
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
340 345 350

<210> 59  
<211> 1056  
<212> DNA  
<213> Tomato golden mosaic virus

<220>  
<221> CDS  
<222> (1)..(1056)  
<223> TGMV AL1 ND133 (Ala3) mutant

<400> 59  
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48  
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96  
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144  
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag	192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	
50 55 60	
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta	240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	
65 70 75 80	
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc	384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	
115 120 125	
caa aca tct gcg gcc gct gca gca gag gcg tta aat gct tct tcc aaa	432
Gln Thr Ser Ala Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	
130 135 140	
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta	480
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	
145 150 155 160	
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn  
 275 280 285

tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc 912  
 Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile  
 290 295 300

gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac 960  
 Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
 305 310 315 320

aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa 1008  
 Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
 325 330 335

ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc 1056  
 Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
 340 345 350

<210> 60  
 <211> 352  
 <212> PRT  
 <213> Tomato golden mosaic virus

<400> 60

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
 1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
 20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
 35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
 50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
 65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
 115 120 125

Gln Thr Ser Ala Ala Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys  
 130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser  
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp  
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn  
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys  
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu  
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn  
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile  
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
 340 345 350

<210> 61  
 <211> 1056  
 <212> DNA  
 <213> Tomato golden mosaic virus

<220>  
 <221> CDS  
 <222> (1)..(1056)  
 <223> TGMV AL1 E--N140 (Ala4) mutant

<400> 61  
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48  
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
 1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96  
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
 20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144  
 Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
 35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192  
 Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
 50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240  
 Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
 65 70 75 80

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288  
 Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
 85 90 95

tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336  
 Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
 100 105 110

gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384  
 Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
 115 120 125

caa aca tct aac gac gct gca gcg gcc gcg tta gct gct tct tcc aaa 432  
 Gln Thr Ser Asn Asp Ala Ala Ala Ala Ala Leu Ala Ala Ser Ser Lys  
 130 135 140

gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta 480  
 Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
 145 150 155 160

ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag 528  
 Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
 165 170 175



act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt ccg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 62  
 <211> 352  
 <212> PRT  
 <213> Tomato golden mosaic virus

<400> 62

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln

20	25	30
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys		
35	40	45
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln		
50	55	60
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val		
65	70	75
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys		
	85	90
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu		
	100	105
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys		
	115	120
Gln Thr Ser Asn Asp Ala Ala Ala Ala Ala Leu Ala Ala Ser Ser Lys		
	130	135
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu		
145	150	155
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys		
	165	170
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn		
	180	185
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser		
	195	200
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp		
210	215	220
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn		
225	230	235
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys		
	245	250
		255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu  
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn  
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile  
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
 340 345 350

<210> 63  
 <211> 1056  
 <212> DNA  
 <213> Tomato golden mosaic virus

<220>  
 <221> CDS  
 <222> (1)..(1056)  
 <223> TGMV AL1 KEE146 (Ala5) mutant

<400> 63  
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48  
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
 1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96  
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
 20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144  
 Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
 35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192  
 Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
 50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240  
 Phe Glu Gly Lys Tyr Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
 65 70 75 80

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc	384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	
115 120 125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc gcg	432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Ala	
130 135 140	
gcc gca gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta	480
Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	
145 150 155 160	
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	

gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac 960  
 Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
 305 310 315 320

aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa 1008  
 Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
 325 330 335

ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc 1056  
 Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
 340 345 350

<210> 64

<211> 352

<212> PRT

<213> Tomato golden mosaic virus

<400> 64

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
 1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
 20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
 35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
 50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
 65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Ala  
 130 135 140

Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu

145		150		155		160									
Phe	Gln	Phe	His	Asn	Leu	Asn	Ser	Asn	Leu	Asp	Arg	Ile	Phe	Asp	Lys
				165					170					175	
Thr	Pro	Glu	Pro	Trp	Leu	Pro	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn
			180					185					190		
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr	Phe	Gly	Lys	Ser
		195					200					205			
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Ile	Glu	Gly	Asp
	210					215					220				
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn
225					230					235					240
Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys
				245					250					255	
Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu
			260					265					270		
Lys	His	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn
		275					280					285			
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile
	290					295					300				
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp
305					310					315					320
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys
				325					330					335	
Phe	Val	Phe	Leu	Asn	Ser	Pro	Leu	Tyr	Gln	Ser	Ser	Thr	Gln	Ser	Ser
			340					345					350		

<210> 65  
 <211> 1056  
 <212> DNA  
 <213> Tomato golden mosaic virus

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<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV AL1 REK154 (Ala6) mutant

<400> 65
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt      48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1          5          10          15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa      96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
          20          25          30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc      144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
          35          40          45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag      192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
          50          55          60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta      240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65          70          75          80

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa      288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
          85          90          95

tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt      336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
          100          105          110

gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc      384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
          115          120          125

caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa      432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
          130          135          140

gaa gaa gcc ctg cag ata att gcg gcc gca atc cca gaa aaa tat tta      480
Glu Glu Ala Leu Gln Ile Ile Ala Ala Ala Ile Pro Glu Lys Tyr Leu
145          150          155          160

ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag      528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
          165          170          175

act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac      576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
          180          185          190

gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt      624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser
          195          200          205

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tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	

agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	

tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	

gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	

aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	

tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	

gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	

aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	

ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 66

<211> 352

<212> PRT

<213> Tomato golden mosaic virus

<400> 66

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45



Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
 50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
 65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys  
 130 135 140

Glu Glu Ala Leu Gln Ile Ile Ala Ala Ala Ile Pro Glu Lys Tyr Leu  
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser  
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp  
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn  
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys  
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu  
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn

275		280		285
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile				
290		295		300
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp				
305		310		315 320
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys				
		325		330 335
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser				
		340		345 350

<210> 67  
 <211> 1056  
 <212> DNA  
 <213> Tomato golden mosaic virus

<220>  
 <221> CDS  
 <222> (1)..(1056)  
 <223> TGMV AL1 EKY159 (Ala7) mutant

<400> 67	
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt	48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe	
1 5 10 15	
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa	96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	
20 25 30	
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc	144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	
35 40 45	
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag	192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	
50 55 60	
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta	240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	
65 70 75 80	
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	

	100	105	110	
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc				384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys				
	115	120	125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa				432
Gln Thr Ser Asn Asp Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys				
	130	135	140	
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gcg gcc gct tta				480
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Ala Ala Ala Leu				
	145	150	155	160
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag				528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys				
	165	170	175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac				576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn				
	180	185	190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt				624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser				
	195	200	205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat				672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp				
	210	215	220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat				720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn				
	225	230	235	240
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag				768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys				
	245	250	255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg				816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu				
	260	265	270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac				864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn				
	275	280	285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc				912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile				
	290	295	300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac				960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp				
	305	310	315	320
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa				1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys				
	325	330	335	

ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc 1056  
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
340 345 350

<210> 68  
<211> 352  
<212> PRT  
<213> Tomato golden mosaic virus

<400> 68

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys  
130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Ala Ala Ala Leu  
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser  
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp  
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn  
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys  
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu  
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn  
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile  
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
340 345 350

<210> 69  
<211> 1056  
<212> DNA  
<213> Tomato golden mosaic virus

<220>  
<221> CDS  
<222> (1)..(1056)  
<223> TGMV AL1 Q-HN165 (Ala8) mutant

<400> 69  
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt

48

Met	Pro	Ser	His	Pro	Lys	Arg	Phe	Gln	Ile	Asn	Ala	Lys	Asn	Tyr	Phe		
1				5					10					15			
ctt	aca	tat	cct	cag	tgc	tcc	ttg	tcc	aaa	gaa	gaa	tca	ctt	tct	caa		96
Leu	Thr	Tyr	Pro	Gln	Cys	Ser	Leu	Ser	Lys	Glu	Glu	Ser	Leu	Ser	Gln		
			20					25					30				
tta	caa	gcc	cta	aac	act	ccg	att	aac	aaa	aaa	ttc	ata	aaa	atc	tgc		144
Leu	Gln	Ala	Leu	Asn	Thr	Pro	Ile	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys		
		35					40					45					
aga	gag	ctt	cat	gaa	gat	ggg	caa	cct	cac	ctc	cac	gtg	ctt	att	cag		192
Arg	Glu	Leu	His	Glu	Asp	Gly	Gln	Pro	His	Leu	His	Val	Leu	Ile	Gln		
	50					55					60						
ttc	gag	gga	aaa	tac	tgc	tgc	caa	aat	caa	cga	ttc	ttc	gac	ctg	gta		240
Phe	Glu	Gly	Lys	Tyr	Cys	Cys	Gln	Asn	Gln	Arg	Phe	Phe	Asp	Leu	Val		
65					70					75				80			
tcc	cca	aca	agg	tca	gca	cat	ttc	cat	cca	aac	att	cag	aga	gct	aaa		288
Ser	Pro	Thr	Arg	Ser	Ala	His	Phe	His	Pro	Asn	Ile	Gln	Arg	Ala	Lys		
				85					90					95			
tcg	tct	tcc	gac	gtc	aag	acg	tac	atc	gac	aaa	gac	gga	gat	act	ctt		336
Ser	Ser	Ser	Asp	Val	Lys	Thr	Tyr	Ile	Asp	Lys	Asp	Gly	Asp	Thr	Leu		
			100					105					110				
gta	tggt	gga	gaa	ttc	cag	gtc	gac	ggg	cga	agt	gct	aga	gga	ggg	tgc		384
Val	Trp	Gly	Glu	Phe	Gln	Val	Asp	Gly	Arg	Ser	Ala	Arg	Gly	Gly	Cys		
		115				120						125					
caa	aca	tct	aac	gac	gct	gca	gca	gag	gcg	tta	aat	gct	tct	tcc	aaa		432
Gln	Thr	Ser	Asn	Asp	Ala	Ala	Ala	Glu	Ala	Leu	Asn	Ala	Ser	Ser	Lys		
	130					135					140						
gaa	gaa	gcc	ctg	cag	ata	att	aga	gag	aaa	atc	cca	gaa	aaa	tat	tta		480
Glu	Glu	Ala	Leu	Gln	Ile	Ile	Arg	Glu	Lys	Ile	Pro	Glu	Lys	Tyr	Leu		
145					150				155						160		
ttt	gcg	ttc	gcc	gct	cta	aat	agc	aat	tta	gat	agg	ata	ttt	gat	aag		528
Phe	Ala	Phe	Ala	Ala	Leu	Asn	Ser	Asn	Leu	Asp	Arg	Ile	Phe	Asp	Lys		
				165					170					175			
act	cct	gaa	cca	tggt	ctt	cct	ccg	ttc	cac	gtc	tca	tca	ttt	act	aac		576
Thr	Pro	Glu	Pro	Trp	Leu	Pro	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn		
			180					185					190				
gtg	cca	gac	gag	atg	aga	caa	tggt	gct	gaa	aat	tat	ttt	gga	aag	agt		624
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr	Phe	Gly	Lys	Ser		
		195				200						205					
tcc	gct	gcg	cgg	ccg	gag	aga	cct	att	agt	att	atc	atc	gag	ggc	gat		672
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Ile	Glu	Gly	Asp		
	210					215					220						
agt	cgg	acg	gga	aag	act	atg	tggt	gct	cgt	tca	cta	ggc	cca	cat	aat		720
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn		

225	230	235	240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag				768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	245	250	255	
ggt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg				816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	260	265	270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac				864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	275	280	285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc				912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	290	295	300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac				960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	305	310	315	320
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa				1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	325	330	335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc				1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	340	345	350	

<210> 70  
 <211> 352  
 <212> PRT  
 <213> Tomato golden mosaic virus

<400> 70

Met	Pro	Ser	His	Pro	Lys	Arg	Phe	Gln	Ile	Asn	Ala	Lys	Asn	Tyr	Phe
1				5					10					15	

Leu	Thr	Tyr	Pro	Gln	Cys	Ser	Leu	Ser	Lys	Glu	Glu	Ser	Leu	Ser	Gln
			20					25					30		

Leu	Gln	Ala	Leu	Asn	Thr	Pro	Ile	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys
		35					40					45			

Arg	Glu	Leu	His	Glu	Asp	Gly	Gln	Pro	His	Leu	His	Val	Leu	Ile	Gln
	50					55				60					

Phe	Glu	Gly	Lys	Tyr	Cys	Cys	Gln	Asn	Gln	Arg	Phe	Phe	Asp	Leu	Val
65					70					75				80	

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys  
 130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
 145 150 155 160

Phe Ala Phe Ala Ala Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser  
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp  
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn  
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys  
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu  
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn  
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile  
 290 295 300



Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
340 345 350

<210> 71  
<211> 1056  
<212> DNA  
<213> Tomato golden mosaic virus

<220>  
<221> CDS  
<222> (1)..(1056)  
<223> TGMV AL1 N-DR172 (Ala9) mutant

<400> 71  
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48  
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
1 5 10 15  
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96  
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
20 25 30  
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144  
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
35 40 45  
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192  
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
50 55 60  
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240  
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
65 70 75 80  
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288  
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
85 90 95  
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336  
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
100 105 110  
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384  
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
115 120 125  
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa 432

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	
130 135 140	
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta	480
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	
145 150 155 160	
ttt cag ttc cac aat cta aat agc gcg cta gct gcg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Ala Leu Ala Ala Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 72

<211> 352  
 <212> PRT  
 <213> Tomato golden mosaic virus

<400> 72

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
 1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
 20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
 35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
 50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
 65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys  
 130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Ala Leu Ala Ala Ile Phe Asp Lys  
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser  
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp  
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn  
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys  
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu  
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn  
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile  
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
 340 345 350

<210> 73  
 <211> 1056  
 <212> DNA  
 <213> Tomato golden mosaic virus

<220>  
 <221> CDS  
 <222> (1)..(1056)  
 <223> TGMV AL1 K--E179 (Ala10) mutant

<400> 73  
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48  
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
 1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96  
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
 20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc	144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	
35 40 45	
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag	192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	
50 55 60	
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta	240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	
65 70 75 80	
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc	384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	
115 120 125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa	432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	
130 135 140	
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta	480
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	
145 150 155 160	
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat gcg	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Ala	
165 170 175	
act ccg gcg cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Ala Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816

Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu		
			260					265					270				
aaa	cat	tgg	aaa	gaa	ctc	att	ggg	gcc	caa	aga	gat	tgg	cag	act	aac		864
Lys	His	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn		
			275				280					285					
tgt	aaa	tac	gga	aag	cca	gtt	caa	att	aaa	gga	ggt	atc	ccg	tca	atc		912
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile		
			290				295				300						
gtg	ctg	tgc	aat	cct	gga	gag	ggg	gct	agc	tat	aaa	gtt	ttc	ctc	gac		960
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp		
						310				315					320		
aaa	gag	gaa	aac	act	cca	cta	aag	aac	tgg	act	ttc	cat	aat	gcg	aaa		1008
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys		
				325				330						335			
ttc	gtc	ttc	ctc	aac	tcc	ccc	ctc	tat	caa	agc	tca	aca	cag	agc	agc		1056
Phe	Val	Phe	Leu	Asn	Ser	Pro	Leu	Tyr	Gln	Ser	Ser	Thr	Gln	Ser	Ser		
			340					345					350				

<210> 74  
 <211> 352  
 <212> PRT  
 <213> Tomato golden mosaic virus

<400> 74

Met	Pro	Ser	His	Pro	Lys	Arg	Phe	Gln	Ile	Asn	Ala	Lys	Asn	Tyr	Phe
1				5					10					15	

Leu	Thr	Tyr	Pro	Gln	Cys	Ser	Leu	Ser	Lys	Glu	Glu	Ser	Leu	Ser	Gln
			20					25					30		

Leu	Gln	Ala	Leu	Asn	Thr	Pro	Ile	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys
		35					40					45			

Arg	Glu	Leu	His	Glu	Asp	Gly	Gln	Pro	His	Leu	His	Val	Leu	Ile	Gln
	50					55					60				

Phe	Glu	Gly	Lys	Tyr	Cys	Cys	Gln	Asn	Gln	Arg	Phe	Phe	Asp	Leu	Val
65					70					75				80	

Ser	Pro	Thr	Arg	Ser	Ala	His	Phe	His	Pro	Asn	Ile	Gln	Arg	Ala	Lys
				85					90					95	

Ser	Ser	Ser	Asp	Val	Lys	Thr	Tyr	Ile	Asp	Lys	Asp	Gly	Asp	Thr	Leu
			100					105					110		

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys  
130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Ala  
165 170 175

Thr Pro Ala Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser  
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp  
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn  
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys  
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu  
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn  
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile  
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
340 345 350

<210> 75  
<211> 1056  
<212> DNA  
<213> Tomato golden mosaic virus

<220>  
<221> CDS  
<222> (1)..(1056)  
<223> TGMV AL1 AAA136 (Leu) mutant

<400> 75  
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48  
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
1 5 10 15  
  
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96  
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
20 25 30  
  
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144  
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
35 40 45  
  
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192  
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
50 55 60  
  
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240  
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
65 70 75 80  
  
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288  
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
85 90 95  
  
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336  
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
100 105 110  
  
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384  
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
115 120 125  
  
caa aca tct aac gac ctt cta cta gag gcc tta aat gct tct tcc aaa 432  
Gln Thr Ser Asn Asp Leu Leu Leu Glu Ala Leu Asn Ala Ser Ser Lys  
130 135 140  
  
gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta 480  
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
145 150 155 160



ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 76

<211> 352

<212> PRT

<213> Tomato golden mosaic virus

<400> 76

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe

1	5	10	15
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	20	25	30
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	35	40	45
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	50	55	60
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	65	70	80
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	85	90	95
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	100	105	110
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	115	120	125
Gln Thr Ser Asn Asp Leu Leu Leu Glu Ala Leu Asn Ala Ser Ser Lys	130	135	140
Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	145	150	155
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	165	170	175
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	180	185	190
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	195	200	205
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	210	215	220
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	225	230	235
			240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys  
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu  
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn  
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile  
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
340 345 350

<210> 77  
<211> 1056  
<212> DNA  
<213> Tomato golden mosaic virus

<220>  
<221> CDS  
<222> (1)..(1056)  
<223> TGMV AL1 E--N140 + KEE146 (Ala4+5) mutant

<400> 77  
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48  
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
1 5 10 15  
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96  
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
20 25 30  
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144  
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
35 40 45  
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192  
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta	240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	
65 70 75 80	
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc	384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	
115 120 125	
caa aca tct aac gac gct gca gcg gcc gcg tta gct gct tct tcc gcg	432
Gln Thr Ser Asn Asp Ala Ala Ala Ala Ala Leu Ala Ala Ser Ser Ala	
130 135 140	
gcc gca gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta	480
Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	
145 150 155 160	
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	

tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc 912  
 Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile  
 290 295 300

gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac 960  
 Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
 305 310 315 320

aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa 1008  
 Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
 325 330 335

ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc 1056  
 Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
 340 345 350

<210> 78

<211> 352

<212> PRT

<213> Tomato golden mosaic virus

<400> 78

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
 1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
 20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
 35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
 50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
 65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Ala Ala Leu Ala Ala Ser Ser Ala

130		135		140
Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu				
145		150		155 160
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys				
	165		170	175
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn				
	180		185	190
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser				
	195		200	205
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp				
	210		215	220
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn				
	225		230	235 240
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys				
	245		250	255
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu				
	260		265	270
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn				
	275		280	285
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile				
	290		295	300
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp				
	305		310	315 320
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys				
	325		330	335
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser				
	340		345	350

<210> 79  
 <211> 1056

<212> DNA  
 <213> Tomato golden mosaic virus

<220>  
 <221> CDS  
 <222> (1)..(1056)  
 <223> TGMV AL1 K144 mutant

<400> 79  
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48  
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
 1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96  
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
 20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144  
 Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
 35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192  
 Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
 50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240  
 Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
 65 70 75 80

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288  
 Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
 85 90 95

tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336  
 Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
 100 105 110

gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384  
 Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
 115 120 125

caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc gcg 432  
 Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Ala  
 130 135 140

gaa gaa gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta 480  
 Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
 145 150 155 160

ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag 528  
 Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
 165 170 175

act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac 576  
 Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
 180 185 190

gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 80  
 <211> 352  
 <212> PRT  
 <213> Tomato golden mosaic virus

<400> 80

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30



Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
 35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
 50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
 65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Ala  
 130 135 140

Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser  
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp  
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn  
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys  
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu

260	265	270
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn		
275	280	285
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile		
290	295	300
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp		
305	310	315 320
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys		
325	330	335
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser		
340	345	350

<210> 81  
 <211> 1056  
 <212> DNA  
 <213> Tomato golden mosaic virus

<220>  
 <221> CDS  
 <222> (1)..(1056)  
 <223> TGMV AL1 E145 mutant

<400> 81	
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt	48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe	
1 5 10 15	
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa	96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	
20 25 30	
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc	144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	
35 40 45	
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag	192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	
50 55 60	
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta	240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	
65 70 75 80	
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	

85										90					95					
tcg	tct	tcc	gac	gtc	aag	acg	tac	atc	gac	aaa	gac	gga	gat	act	ctt	336				
Ser	Ser	Ser	Asp	Val	Lys	Thr	Tyr	Ile	Asp	Lys	Asp	Gly	Asp	Thr	Leu					
100					105					110										
gta	tgg	gga	gaa	ttc	cag	gtc	gac	ggg	cga	agt	gct	aga	gga	ggg	tgc	384				
Val	Trp	Gly	Glu	Phe	Gln	Val	Asp	Gly	Arg	Ser	Ala	Arg	Gly	Gly	Cys					
115					120					125										
caa	aca	tct	aac	gac	gct	gca	gca	gag	gcg	tta	aat	gct	tct	tcc	aaa	432				
Gln	Thr	Ser	Asn	Asp	Ala	Ala	Ala	Glu	Ala	Leu	Asn	Ala	Ser	Ser	Lys					
130					135					140										
gca	gag	gcc	ctg	cag	ata	att	aga	gag	aaa	atc	cca	gaa	aaa	tat	tta	480				
Ala	Glu	Ala	Leu	Gln	Ile	Ile	Arg	Glu	Lys	Ile	Pro	Glu	Lys	Tyr	Leu					
145					150					155					160					
ttt	cag	ttc	cac	aat	cta	aat	agc	aat	tta	gat	agg	ata	ttt	gat	aag	528				
Phe	Gln	Phe	His	Asn	Leu	Asn	Ser	Asn	Leu	Asp	Arg	Ile	Phe	Asp	Lys					
165					170					175										
act	cct	gaa	cca	tgg	ctt	cct	ccg	ttc	cac	gtc	tca	tca	ttt	act	aac	576				
Thr	Pro	Glu	Pro	Trp	Leu	Pro	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn					
180					185					190										
gtg	cca	gac	gag	atg	aga	caa	tgg	gct	gaa	aat	tat	ttt	gga	aag	agt	624				
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr	Phe	Gly	Lys	Ser					
195					200					205										
tcc	gct	gcg	cgg	ccg	gag	aga	cct	att	agt	att	atc	atc	gag	ggc	gat	672				
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Ile	Glu	Gly	Asp					
210					215					220										
agt	cgg	acg	gga	aag	act	atg	tgg	gct	cgt	tca	cta	ggc	cca	cat	aat	720				
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn					
225					230					235					240					
tat	ttg	agc	ggg	cat	ttg	gat	ctc	aat	tct	agg	gtt	tac	tca	aac	aag	768				
Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys					
245					250					255										
gtt	gag	tat	aac	gtc	atc	gat	gat	gtc	aca	ccg	caa	tat	cta	aag	ttg	816				
Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu					
260					265					270										
aaa	cat	tgg	aaa	gaa	ctc	att	ggg	gcc	caa	aga	gat	tgg	cag	act	aac	864				
Lys	His	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn					
275					280					285										
tgt	aaa	tac	gga	aag	cca	gtt	caa	att	aaa	gga	ggg	atc	ccg	tca	atc	912				
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile					
290					295					300										
gtg	ctg	tgc	aat	cct	gga	gag	ggg	gct	agc	tat	aaa	gtt	ttc	ctc	gac	960				
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp					
305					310					315					320					

aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	

ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 82  
 <211> 352  
 <212> PRT  
 <213> Tomato golden mosaic virus

<400> 82

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
130 135 140

Ala Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser  
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp  
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn  
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys  
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu  
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn  
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile  
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
340 345 350

<210> 83  
<211> 1056  
<212> DNA  
<213> Tomato golden mosaic virus

<220>  
<221> CDS  
<222> (1) .. (1056)

<223> TGMV AL1 E146 mutant

<400> 83

atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt	48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe	
1 5 10 15	
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa	96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	
20 25 30	
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc	144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	
35 40 45	
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag	192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	
50 55 60	
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta	240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	
65 70 75 80	
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc	384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	
115 120 125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa	432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	
130 135 140	
gaa gca gcc ctg cag ata att aga gag aaa atc cca gaa aaa tat tta	480
Glu Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	
145 150 155 160	
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	

210	215	220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat			720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn			
225	230	235	240
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag			768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys			
	245	250	255
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg			816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu			
	260	265	270
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac			864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn			
	275	280	285
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc			912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile			
	290	295	300
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac			960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp			
	305	310	315
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa			1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys			
	325	330	335
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc			1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser			
	340	345	350

<210> 84  
 <211> 352  
 <212> PRT  
 <213> Tomato golden mosaic virus

<400> 84

Met	Pro	Ser	His	Pro	Lys	Arg	Phe	Gln	Ile	Asn	Ala	Lys	Asn	Tyr	Phe
1				5					10					15	

Leu	Thr	Tyr	Pro	Gln	Cys	Ser	Leu	Ser	Lys	Glu	Glu	Ser	Leu	Ser	Gln
			20						25					30	

Leu	Gln	Ala	Leu	Asn	Thr	Pro	Ile	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys
		35					40					45			

Arg	Glu	Leu	His	Glu	Asp	Gly	Gln	Pro	His	Leu	His	Val	Leu	Ile	Gln
	50					55					60				

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys  
130 135 140

Glu Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser  
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp  
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn  
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys  
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu  
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn  
275 280 285



Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile  
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
 340 345 350

<210> 85  
 <211> 1056  
 <212> DNA  
 <213> Tomato golden mosaic virus

<220>  
 <221> CDS  
 <222> (1)..(1056)  
 <223> TGMV AL1 EE146 mutant

<400> 85  
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48  
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
 1 5 10 15  
 ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96  
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
 20 25 30  
 tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144  
 Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
 35 40 45  
 aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192  
 Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
 50 55 60  
 ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240  
 Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
 65 70 75 80  
 tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288  
 Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
 85 90 95  
 tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336  
 Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
 100 105 110  
 gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384

Val	Trp	Gly	Glu	Phe	Gln	Val	Asp	Gly	Arg	Ser	Ala	Arg	Gly	Gly	Cys	
		115					120					125				
caa	aca	tct	aac	gac	gct	gca	gca	gag	gcg	tta	aat	gct	tct	tcc	aaa	432
Gln	Thr	Ser	Asn	Asp	Ala	Ala	Ala	Glu	Ala	Leu	Asn	Ala	Ser	Ser	Lys	
		130					135				140					
gcg	gcc	gcc	ctg	cag	ata	att	aga	gag	aaa	atc	cca	gaa	aaa	tat	tta	480
Ala	Ala	Ala	Leu	Gln	Ile	Ile	Arg	Glu	Lys	Ile	Pro	Glu	Lys	Tyr	Leu	
145						150				155					160	
ttt	cag	ttc	cac	aat	cta	aat	agc	aat	tta	gat	agg	ata	ttt	gat	aag	528
Phe	Gln	Phe	His	Asn	Leu	Asn	Ser	Asn	Leu	Asp	Arg	Ile	Phe	Asp	Lys	
				165					170					175		
act	cct	gaa	cca	tgg	ctt	cct	ccg	ttc	cac	gtc	tca	tca	ttt	act	aac	576
Thr	Pro	Glu	Pro	Trp	Leu	Pro	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn	
			180					185					190			
gtg	cca	gac	gag	atg	aga	caa	tgg	gct	gaa	aat	tat	ttt	gga	aag	agt	624
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr	Phe	Gly	Lys	Ser	
		195					200					205				
tcc	gct	gcg	cgg	ccg	gag	aga	cct	att	agt	att	atc	atc	gag	ggc	gat	672
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Ile	Glu	Gly	Asp	
		210				215					220					
agt	cgg	acg	gga	aag	act	atg	tgg	gct	cgt	tca	cta	ggc	cca	cat	aat	720
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn	
225					230				235						240	
tat	ttg	agc	ggg	cat	ttg	gat	ctc	aat	tct	agg	gtt	tac	tca	aac	aag	768
Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys	
				245				250						255		
gtt	gag	tat	aac	gtc	atc	gat	gat	gtc	aca	ccg	caa	tat	cta	aag	ttg	816
Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu	
			260					265					270			
aaa	cat	tgg	aaa	gaa	ctc	att	ggg	gcc	caa	aga	gat	tgg	cag	act	aac	864
Lys	His	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn	
		275					280					285				
tgt	aaa	tac	gga	aag	cca	gtt	caa	att	aaa	gga	ggt	atc	ccg	tca	atc	912
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile	
		290				295					300					
gtg	ctg	tgc	aat	cct	gga	gag	ggt	gct	agc	tat	aaa	gtt	ttc	ctc	gac	960
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp	
305					310				315						320	
aaa	gag	gaa	aac	act	cca	cta	aag	aac	tgg	act	ttc	cat	aat	gcg	aaa	1008
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys	
				325				330					335			
ttc	gtc	ttc	ctc	aac	tcc	ccc	ctc	tat	caa	agc	tca	aca	cag	agc	agc	1056
Phe	Val	Phe	Leu	Asn	Ser	Pro	Leu	Tyr	Gln	Ser	Ser	Thr	Gln	Ser	Ser	

340                                      345                                      350  
  
 <210> 86  
 <211> 352  
 <212> PRT  
 <213> Tomato golden mosaic virus  
  
 <400> 86  
  
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
 1                                      5                                      10                                      15  
  
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
                                     20                                      25                                      30  
  
 Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
                                     35                                      40                                      45  
  
 Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
                                     50                                      55                                      60  
  
 Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
 65                                      70                                      75                                      80  
  
 Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
                                     85                                      90                                      95  
  
 Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
                                     100                                      105                                      110  
  
 Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
                                     115                                      120                                      125  
  
 Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys  
                                     130                                      135                                      140  
  
 Ala Ala Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
 145                                      150                                      155                                      160  
  
 Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
                                     165                                      170                                      175  
  
 Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
                                     180                                      185                                      190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser  
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp  
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn  
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys  
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu  
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn  
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile  
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
 340 345 350

<210> 87  
 <211> 1056  
 <212> DNA  
 <213> Tomato golden mosaic virus

<220>  
 <221> CDS  
 <222> (1)..(1056)  
 <223> TGMV AL1 A147Y mutant

<400> 87  
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt  
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
 1 5 10 15

48

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln 20 25 30	96
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys 35 40 45	144
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln 50 55 60	192
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val 65 70 75 80	240
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys 85 90 95	288
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu 100 105 110	336
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys 115 120 125	384
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys 130 135 140	432
gaa gaa tac ctt cag ata att aga gag aaa atc cca gaa aaa tat tta Glu Glu Tyr Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu 145 150 155 160	480
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys 165 170 175	528
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn 180 185 190	576
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser 195 200 205	624
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp 210 215 220	672
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn 225 230 235 240	720
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768

Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys	
				245					250					255		
ggt	gag	tat	aac	gtc	atc	gat	gat	gtc	aca	ccg	caa	tat	cta	aag	ttg	816
Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu	
			260					265					270			
aaa	cat	tgg	aaa	gaa	ctc	att	ggg	gcc	caa	aga	gat	tgg	cag	act	aac	864
Lys	His	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn	
		275					280					285				
tgt	aaa	tac	gga	aag	cca	gtt	caa	att	aaa	gga	ggt	atc	ccg	tca	atc	912
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile	
	290					295					300					
gtg	ctg	tgc	aat	cct	gga	gag	ggt	gct	agc	tat	aaa	gtt	ttc	ctc	gac	960
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp	
305					310				315						320	
aaa	gag	gaa	aac	act	cca	cta	aag	aac	tgg	act	ttc	cat	aat	gcg	aaa	1008
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys	
			325					330						335		
ttc	gtc	ttc	ctc	aac	tcc	ccc	ctc	tat	caa	agc	tca	aca	cag	agc	agc	1056
Phe	Val	Phe	Leu	Asn	Ser	Pro	Leu	Tyr	Gln	Ser	Ser	Thr	Gln	Ser	Ser	
			340					345					350			

<210> 88  
 <211> 352  
 <212> PRT  
 <213> Tomato golden mosaic virus

<400> 88

Met	Pro	Ser	His	Pro	Lys	Arg	Phe	Gln	Ile	Asn	Ala	Lys	Asn	Tyr	Phe
1				5					10					15	
Leu	Thr	Tyr	Pro	Gln	Cys	Ser	Leu	Ser	Lys	Glu	Glu	Ser	Leu	Ser	Gln
			20					25					30		
Leu	Gln	Ala	Leu	Asn	Thr	Pro	Ile	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys
		35					40					45			
Arg	Glu	Leu	His	Glu	Asp	Gly	Gln	Pro	His	Leu	His	Val	Leu	Ile	Gln
	50					55					60				
Phe	Glu	Gly	Lys	Tyr	Cys	Cys	Gln	Asn	Gln	Arg	Phe	Phe	Asp	Leu	Val
65					70					75				80	
Ser	Pro	Thr	Arg	Ser	Ala	His	Phe	His	Pro	Asn	Ile	Gln	Arg	Ala	Lys
				85					90					95	

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys  
 130 135 140

Glu Glu Tyr Leu Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser  
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp  
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn  
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys  
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu  
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn  
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile  
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
 340 345 350

<210> 89  
 <211> 1056  
 <212> DNA  
 <213> Tomato golden mosaic virus

<220>  
 <221> CDS  
 <222> (1)..(1056)  
 <223> TGMV AL1 L148 mutant

<400> 89  
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48  
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
 1 5 10 15  
 ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96  
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
 20 25 30  
 tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144  
 Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
 35 40 45  
 aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192  
 Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
 50 55 60  
 ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240  
 Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
 65 70 75 80  
 tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288  
 Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
 85 90 95  
 tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336  
 Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
 100 105 110  
 gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384  
 Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
 115 120 125  
 caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa 432  
 Gln Thr Ser Asn Asp Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys  
 130 135 140



gaa gaa gct gcg cag ata att aga gag aaa atc cca gaa aaa tat tta	480
Glu Glu Ala Ala Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	
145 150 155 160	
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 90  
 <211> 352  
 <212> PRT  
 <213> Tomato golden mosaic virus

<400> 90

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys  
130 135 140

Glu Glu Ala Ala Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser  
195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp  
210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn  
225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys  
245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu  
260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn  
275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile  
290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
340 345 350

<210> 91  
<211> 1056  
<212> DNA  
<213> Tomato golden mosaic virus

<220>  
<221> CDS  
<222> (1)..(1056)  
<223> TGMV AL1 L148V mutant

<400> 91  
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48  
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96  
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144  
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag	192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	
50 55 60	
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta	240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	
65 70 75 80	
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa	288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys	
85 90 95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt	336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu	
100 105 110	
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc	384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys	
115 120 125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa	432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys	
130 135 140	
gaa gag gcc gtg cag ata att aga gag aaa atc cca gaa aaa tat tta	480
Glu Glu Ala Val Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu	
145 150 155 160	
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag	528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys	
165 170 175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	

aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	

tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	

gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	

aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	

ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 92  
 <211> 352  
 <212> PRT  
 <213> Tomato golden mosaic virus

<400> 92

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15

Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
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115					120					125						
Gln	Thr	Ser	Asn	Asp	Ala	Ala	Ala	Glu	Ala	Leu	Asn	Ala	Ser	Ser	Lys	
130					135					140						
Glu	Glu	Ala	Val	Gln	Ile	Ile	Arg	Glu	Lys	Ile	Pro	Glu	Lys	Tyr	Leu	
145					150					155					160	
Phe	Gln	Phe	His	Asn	Leu	Asn	Ser	Asn	Leu	Asp	Arg	Ile	Phe	Asp	Lys	
165					170					175						
Thr	Pro	Glu	Pro	Trp	Leu	Pro	Pro	Phe	His	Val	Ser	Ser	Phe	Thr	Asn	
180					185					190						
Val	Pro	Asp	Glu	Met	Arg	Gln	Trp	Ala	Glu	Asn	Tyr	Phe	Gly	Lys	Ser	
195					200					205						
Ser	Ala	Ala	Arg	Pro	Glu	Arg	Pro	Ile	Ser	Ile	Ile	Ile	Glu	Gly	Asp	
210					215					220						
Ser	Arg	Thr	Gly	Lys	Thr	Met	Trp	Ala	Arg	Ser	Leu	Gly	Pro	His	Asn	
225					230					235					240	
Tyr	Leu	Ser	Gly	His	Leu	Asp	Leu	Asn	Ser	Arg	Val	Tyr	Ser	Asn	Lys	
245					250					255						
Val	Glu	Tyr	Asn	Val	Ile	Asp	Asp	Val	Thr	Pro	Gln	Tyr	Leu	Lys	Leu	
260					265					270						
Lys	His	Trp	Lys	Glu	Leu	Ile	Gly	Ala	Gln	Arg	Asp	Trp	Gln	Thr	Asn	
275					280					285						
Cys	Lys	Tyr	Gly	Lys	Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ser	Ile	
290					295					300						
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp	
305					310					315					320	
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys	
325					330					335						
Phe	Val	Phe	Leu	Asn	Ser	Pro	Leu	Tyr	Gln	Ser	Ser	Thr	Gln	Ser	Ser	
340					345					350						

<210> 93  
 <211> 1056  
 <212> DNA  
 <213> Tomato golden mosaic virus

<220>  
 <221> CDS  
 <222> (1)..(1056)  
 <223> TGMV AL1 L148V\* mutant

<400> 93  
 atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt 48  
 Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe  
 1 5 10 15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa 96  
 Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
 20 25 30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc 144  
 Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
 35 40 45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag 192  
 Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
 50 55 60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta 240  
 Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
 65 70 75 80

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa 288  
 Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
 85 90 95

tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt 336  
 Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
 100 105 110

gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc 384  
 Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
 115 120 125

caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa 432  
 Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys  
 130 135 140

gaa gaa gcc gtt cag ata att aga gag aaa atc cca gaa aaa tat tta 480  
 Glu Glu Ala Val Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
 145 150 155 160

ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag 528  
 Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
 165 170 175

act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac	576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn	
180 185 190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt	624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser	
195 200 205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat	672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp	
210 215 220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat	720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn	
225 230 235 240	
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag	768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys	
245 250 255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg	816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu	
260 265 270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac	864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn	
275 280 285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc	912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile	
290 295 300	
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac	960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp	
305 310 315 320	
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa	1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys	
325 330 335	
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc	1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser	
340 345 350	

<210> 94  
 <211> 352  
 <212> PRT  
 <213> Tomato golden mosaic virus

<400> 94

Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1 5 10 15



Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln  
 20 25 30

Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys  
 35 40 45

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
 50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
 65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys  
 130 135 140

Glu Glu Ala Val Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser  
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp  
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn  
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys

	245		250		255
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu					
	260		265		270
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn					
	275		280		285
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile					
	290		295		300
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp					
	305		310		315
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys					
	325		330		335
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser					
	340		345		350

<210> 95  
 <211> 1056  
 <212> DNA  
 <213> Tomato golden mosaic virus

<220>  
 <221> CDS  
 <222> (1)..(1056)  
 <223> TGMV AL1 L148G mutant

<400> 95	
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt	48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe	
1 5 10 15	
ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa	96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln	
20 25 30	
tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc	144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys	
35 40 45	
aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag	192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln	
50 55 60	
ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta	240
Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val	

65		70		75		80	
tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa							288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys							
	85			90		95	
tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt							336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu							
	100			105		110	
gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc							384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys							
	115			120		125	
caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa							432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys							
	130			135		140	
gaa gaa gcc ggc cag ata att aga gag aaa atc cca gaa aaa tat tta							480
Glu Glu Ala Gly Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu							
	145			150		155	160
ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag							528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys							
	165			170		175	
act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac							576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn							
	180			185		190	
gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt							624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser							
	195			200		205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat							672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp							
	210			215		220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat							720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn							
	225			230		235	240
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag							768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys							
	245			250		255	
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg							816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu							
	260			265		270	
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac							864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn							
	275			280		285	
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc							912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile							
	290			295		300	

gtg	ctg	tgc	aat	cct	gga	gag	ggt	gct	agc	tat	aaa	gtt	ttc	ctc	gac	960
Val	Leu	Cys	Asn	Pro	Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Val	Phe	Leu	Asp	
305					310				315						320	

aaa	gag	gaa	aac	act	cca	cta	aag	aac	tgg	act	ttc	cat	aat	gcg	aaa	1008
Lys	Glu	Glu	Asn	Thr	Pro	Leu	Lys	Asn	Trp	Thr	Phe	His	Asn	Ala	Lys	
			325					330						335		

ttc	gtc	ttc	ctc	aac	tcc	ccc	ctc	tat	caa	agc	tca	aca	cag	agc	agc	1056
Phe	Val	Phe	Leu	Asn	Ser	Pro	Leu	Tyr	Gln	Ser	Ser	Thr	Gln	Ser	Ser	
			340					345					350			

<210> 96  
 <211> 352  
 <212> PRT  
 <213> Tomato golden mosaic virus

<400> 96

Met	Pro	Ser	His	Pro	Lys	Arg	Phe	Gln	Ile	Asn	Ala	Lys	Asn	Tyr	Phe
1				5					10					15	

Leu	Thr	Tyr	Pro	Gln	Cys	Ser	Leu	Ser	Lys	Glu	Glu	Ser	Leu	Ser	Gln
			20					25					30		

Leu	Gln	Ala	Leu	Asn	Thr	Pro	Ile	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys
		35					40					45			

Arg	Glu	Leu	His	Glu	Asp	Gly	Gln	Pro	His	Leu	His	Val	Leu	Ile	Gln
	50					55					60				

Phe	Glu	Gly	Lys	Tyr	Cys	Cys	Gln	Asn	Gln	Arg	Phe	Phe	Asp	Leu	Val
65					70					75				80	

Ser	Pro	Thr	Arg	Ser	Ala	His	Phe	His	Pro	Asn	Ile	Gln	Arg	Ala	Lys
				85					90					95	

Ser	Ser	Ser	Asp	Val	Lys	Thr	Tyr	Ile	Asp	Lys	Asp	Gly	Asp	Thr	Leu
			100					105					110		

Val	Trp	Gly	Glu	Phe	Gln	Val	Asp	Gly	Arg	Ser	Ala	Arg	Gly	Gly	Cys
		115					120					125			

Gln	Thr	Ser	Asn	Asp	Ala	Ala	Ala	Glu	Ala	Leu	Asn	Ala	Ser	Ser	Lys
	130					135					140				

Glu Glu Ala Gly Gln Ile Ile Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser  
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp  
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn  
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys  
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu  
 260 265 270

Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn  
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile  
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
 340 345 350

<210> 97

<211> 1056

<212> DNA

<213> Tomato golden mosaic virus

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<220>
<221> CDS
<222> (1)..(1056)
<223> TGMV AL1 II151 mutant

<400> 97
atg cca tcg cat cca aaa cgg ttt caa ata aat gcc aaa aat tat ttt      48
Met Pro Ser His Pro Lys Arg Phe Gln Ile Asn Ala Lys Asn Tyr Phe
1          5          10          15

ctt aca tat cct cag tgc tcc ttg tcc aaa gaa gaa tca ctt tct caa      96
Leu Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ser Leu Ser Gln
          20          25          30

tta caa gcc cta aac act ccg att aac aaa aaa ttc ata aaa atc tgc      144
Leu Gln Ala Leu Asn Thr Pro Ile Asn Lys Lys Phe Ile Lys Ile Cys
          35          40          45

aga gag ctt cat gaa gat ggg caa cct cac ctc cac gtg ctt att cag      192
Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln
          50          55          60

ttc gag gga aaa tac tgc tgc caa aat caa cga ttc ttc gac ctg gta      240
Phe Glu Gly Lys Tyr Cys Gln Asn Gln Arg Phe Phe Asp Leu Val
65          70          75          80

tcc cca aca agg tca gca cat ttc cat cca aac att cag aga gct aaa      288
Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys
          85          90          95

tcg tct tcc gac gtc aag acg tac atc gac aaa gac gga gat act ctt      336
Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu
          100          105          110

gta tgg gga gaa ttc cag gtc gac ggt cga agt gct aga gga ggt tgc      384
Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys
          115          120          125

caa aca tct aac gac gct gca gca gag gcg tta aat gct tct tcc aaa      432
Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys
          130          135          140

gaa gaa gcc ctt cag gca gct aga gag aaa atc cca gaa aaa tat tta      480
Glu Glu Ala Leu Gln Ala Ala Arg Glu Lys Ile Pro Glu Lys Tyr Leu
145          150          155          160

ttt cag ttc cac aat cta aat agc aat tta gat agg ata ttt gat aag      528
Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys
          165          170          175

act cct gaa cca tgg ctt cct ccg ttc cac gtc tca tca ttt act aac      576
Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn
          180          185          190

gtg cca gac gag atg aga caa tgg gct gaa aat tat ttt gga aag agt      624
Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser

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195	200	205	
tcc gct gcg cgg ccg gag aga cct att agt att atc atc gag ggc gat			672
Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp			
210	215	220	
agt cgg acg gga aag act atg tgg gct cgt tca cta ggc cca cat aat			720
Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn			
225	230	235	240
tat ttg agc ggg cat ttg gat ctc aat tct agg gtt tac tca aac aag			768
Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys			
	245	250	255
gtt gag tat aac gtc atc gat gat gtc aca ccg caa tat cta aag ttg			816
Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu			
	260	265	270
aaa cat tgg aaa gaa ctc att ggg gcc caa aga gat tgg cag act aac			864
Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn			
	275	280	285
tgt aaa tac gga aag cca gtt caa att aaa gga ggt atc ccg tca atc			912
Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile			
	290	295	300
gtg ctg tgc aat cct gga gag ggt gct agc tat aaa gtt ttc ctc gac			960
Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp			
305	310	315	320
aaa gag gaa aac act cca cta aag aac tgg act ttc cat aat gcg aaa			1008
Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys			
	325	330	335
ttc gtc ttc ctc aac tcc ccc ctc tat caa agc tca aca cag agc agc			1056
Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser			
	340	345	350

<210> 98

<211> 352

<212> PRT

<213> Tomato golden mosaic virus

<400> 98

Met	Pro	Ser	His	Pro	Lys	Arg	Phe	Gln	Ile	Asn	Ala	Lys	Asn	Tyr	Phe
1				5					10					15	

Leu	Thr	Tyr	Pro	Gln	Cys	Ser	Leu	Ser	Lys	Glu	Glu	Ser	Leu	Ser	Gln
			20						25				30		

Leu	Gln	Ala	Leu	Asn	Thr	Pro	Ile	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys
		35					40					45			

Arg Glu Leu His Glu Asp Gly Gln Pro His Leu His Val Leu Ile Gln  
 50 55 60

Phe Glu Gly Lys Tyr Cys Cys Gln Asn Gln Arg Phe Phe Asp Leu Val  
 65 70 75 80

Ser Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Arg Ala Lys  
 85 90 95

Ser Ser Ser Asp Val Lys Thr Tyr Ile Asp Lys Asp Gly Asp Thr Leu  
 100 105 110

Val Trp Gly Glu Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Cys  
 115 120 125

Gln Thr Ser Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys  
 130 135 140

Glu Glu Ala Leu Gln Ala Ala Arg Glu Lys Ile Pro Glu Lys Tyr Leu  
 145 150 155 160

Phe Gln Phe His Asn Leu Asn Ser Asn Leu Asp Arg Ile Phe Asp Lys  
 165 170 175

Thr Pro Glu Pro Trp Leu Pro Pro Phe His Val Ser Ser Phe Thr Asn  
 180 185 190

Val Pro Asp Glu Met Arg Gln Trp Ala Glu Asn Tyr Phe Gly Lys Ser  
 195 200 205

Ser Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Ile Glu Gly Asp  
 210 215 220

Ser Arg Thr Gly Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn  
 225 230 235 240

Tyr Leu Ser Gly His Leu Asp Leu Asn Ser Arg Val Tyr Ser Asn Lys  
 245 250 255

Val Glu Tyr Asn Val Ile Asp Asp Val Thr Pro Gln Tyr Leu Lys Leu  
 260 265 270



Lys His Trp Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Thr Asn  
 275 280 285

Cys Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile  
 290 295 300

Val Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Val Phe Leu Asp  
 305 310 315 320

Lys Glu Glu Asn Thr Pro Leu Lys Asn Trp Thr Phe His Asn Ala Lys  
 325 330 335

Phe Val Phe Leu Asn Ser Pro Leu Tyr Gln Ser Ser Thr Gln Ser Ser  
 340 345 350

<210> 99  
 <211> 25  
 <212> PRT  
 <213> Tomato golden mosaic virus

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(25)  
 <223> Amino acids 132-156 of TGMV AL1

<400> 99

Asn Asp Ala Ala Ala Glu Ala Leu Asn Ala Ser Ser Lys Glu Glu Ala  
 1 5 10 15

Leu Gln Ile Ile Arg Glu Lys Ile Pro  
 20 25

<210> 100  
 <211> 13  
 <212> PRT  
 <213> Tomato golden mosaic virus

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(13)  
 <223> TGMV AL1 amino acids 144-156

<400> 100

Lys Glu Glu Ala Leu Gln Ile Ile Arg Glu Lys Ile Pro  
 1 5 10

<210> 101  
 <211> 13  
 <212> PRT  
 <213> tomato yellow leaf curl virus

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(13)  
 <223> TYLCV C1 amino acids 142-154

<400> 101

Lys Ser Glu Ala Leu Lys Ile Leu Arg Glu Leu Ala Pro  
 1 5 10

<210> 102  
 <211> 13  
 <212> PRT  
 <213> cabbage leaf curl virus

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(13)  
 <223> CbLCV AL1 amino acids 141-153

<400> 102

Val Glu Glu Ala Leu Ala Ile Ile Arg Ala Gly Asp Pro  
 1 5 10

<210> 103  
 <211> 27  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic oligonucleotide primer

<400> 103  
 ggacaccgat tggatccagc atgcctc

27

<210> 104  
 <211> 27  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic oligonucleotide primer

<400> 104  
 ccacagtcga attccccggg cttacgc

27

<210> 105  
 <211> 36  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Mutagenesis oligonucleotide

<400> 105  
 cctaaataag atctacaagg atcccacgaa acccta

36

<210> 106  
 <211> 31  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> CbLCV AL1 L145A mutagenesis oligonucleotide

<400> 106  
 gtgtggaaga ggcgcccgca attataaggg c

31

<210> 107  
 <211> 349  
 <212> PRT  
 <213> cabbage leaf curl virus

<400> 107

Met Pro Arg Asn Pro Lys Ser Phe Arg Leu Ala Ala Arg Asn Ile Phe  
 1 5 10 15

Leu Thr Tyr Pro Gln Cys Asp Ile Pro Lys Asp Glu Ala Leu Gln Met  
 20 25 30

Leu Gln Thr Leu Ser Trp Ser Val Val Lys Pro Thr Tyr Ile Arg Val  
 35 40 45

Ala Arg Glu Glu His Ser Asp Gly Phe Pro His Leu His Cys Leu Ile  
 50 55 60

Gln Leu Ser Gly Lys Ser Asn Ile Lys Asp Ala Arg Phe Phe Asp Ile  
 65 70 75 80

Thr His Pro Arg Arg Ser Ala Asn Phe His Pro Asn Ile Gln Ala Ala  
 85 90 95

Lys Asp Thr Asn Ala Val Lys Asn Tyr Ile Thr Lys Asp Gly Asp Tyr  
 100 105 110

Cys Glu Ser Gly Gln Tyr Lys Val Ser Gly Gly Thr Lys Ala Asn Lys  
 115 120 125

Asp Asp Val Tyr His Asn Ala Val Asn Ala Gly Cys Val Glu Glu Ala  
 130 135 140

Leu Ala Ile Ile Arg Ala Gly Asp Pro Lys Thr Phe Ile Val Ser Tyr  
 145 150 155 160

His Asn Val Arg Ala Asn Ile Glu Arg Leu Phe Thr Lys Ala Pro Glu  
 165 170 175

Pro Trp Ala Pro Pro Phe Gln Leu Ser Ser Phe Thr Asn Val Pro Asp  
 180 185 190

Glu Met Ser Ser Trp Ala Asp Asp Tyr Phe Gly Arg Ser Ala Ala Ala  
 195 200 205

Arg Ala Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser Arg Thr  
 210 215 220

Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr Leu Ser  
 225 230 235 240

Gly His Leu Asp Phe Asn Ser Lys Val Phe Ser Asn Asn Ala Glu Tyr  
 245 250 255

Asn Val Ile Asp Asp Ile Ala Pro His Tyr Leu Lys Leu Lys His Trp  
 260 265 270

Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Ser Asn Cys Lys Tyr  
 275 280 285

Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val Leu Cys  
 290 295 300

Asn Pro Gly Glu Gly Ser Ser Tyr Ile Ser Phe Leu Asn Lys Glu Glu  
 305 310 315 320

Asn Ala Ser Leu Arg Ala Trp Thr Thr Lys Asn Ala Lys Phe Ile Thr

325

330

335

Leu Glu Ala Pro Leu Tyr Gln Ser Thr Ala Gln Asp Cys  
 340 345

<210> 108  
 <211> 70  
 <212> PRT  
 <213> cabbage leaf curl virus

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(70)  
 <223> Wild-type CbLCV AL1 amino acids 111-180

<400> 108

Asp Tyr Cys Glu Ser Gly Gln Tyr Lys Val Ser Gly Gly Thr Lys Ala  
 1 5 10 15

Asn Lys Asp Asp Val Tyr His Asn Ala Val Asn Ala Gly Cys Val Glu  
 20 25 30

Glu Ala Leu Ala Ile Ile Arg Ala Gly Asp Pro Lys Thr Phe Ile Val  
 35 40 45

Ser Tyr His Asn Val Arg Ala Asn Ile Glu Arg Leu Phe Thr Lys Ala  
 50 55 60

Pro Glu Pro Trp Ala Pro  
 65 70

<210> 109  
 <211> 70  
 <212> PRT  
 <213> cabbage leaf curl virus

<220>  
 <221> MISC\_FEATURE  
 <222> (35)..(35)  
 <223> L145A mutation

<400> 109

Asp Tyr Cys Glu Ser Gly Gln Tyr Lys Val Ser Gly Gly Thr Lys Ala  
 1 5 10 15

Asn Lys Asp Asp Val Tyr His Asn Ala Val Asn Ala Gly Cys Val Glu  
 20 25 30

Glu Ala Ala Ala Ile Ile Arg Ala Gly Asp Pro Lys Thr Phe Ile Val  
 35 40 45

Ser Tyr His Asn Val Arg Ala Asn Ile Glu Arg Leu Phe Thr Lys Ala  
 50 55 60

Pro Glu Pro Trp Ala Pro  
 65 70

<210> 110  
 <211> 1047  
 <212> DNA  
 <213> cabbage leaf curl virus

<220>  
 <221> misc\_feature  
 <222> (1)..(1047)  
 <223> CbLCV AL1 coding sequence

<400> 110  
 atgccacgaa accctaaatc gtttcgttta gcagcccgaa atatattctt aacatatccc 60  
 cagtgcgaca tacccaaaga tgaagctctt cagatgcttc aaacctgtc gtggtcagtc 120  
 gtcaaaccga catacatcag agtcgcaaga gaggaacatt cagacgggtt cccccattta 180  
 cactgtctca tccaactatc aggaaagtcg aacatcaagg atgctagatt tttcgacatc 240  
 actcacccca gaaggtctgc caattttcac ccaaacattc aggcagccaa agacaccaat 300  
 gccgtcaaga attacatcac caaagatggg gattattgtg aatccgggca gtacaagggtg 360  
 tctgggggta caaaggcaaa taaagacgac gtctaccaca acgccgtcaa tgcgggatgt 420  
 gtggaagagg ctctcgcaat tataagggct ggagatccaa agacgttcat tgtagttat 480  
 cataatgtta gagctaacat agagcgactc tttactaagg ctccggaacc atgggctcct 540  
 ccgtttcaac tctcctcctt tactaacgac ccggacgaga tgagttcatg ggcagatgac 600  
 tattttgggc ggagtgccgc tgcgcgggcg gaaagaccta ttagtatcat agttgaagg 660  
 gattcacgaa ccggcaagac catgtgggcg cgtgctttag gaccacataa ttatttgagt 720  
 gggcacctcg actttaattc aaaggtcttt tcaaataatg cggagtataa cgtcattgat 780  
 gacatagctc cgcattatct aaagctaaag cactggaaag agcttattgg ggcccaaagg 840  
 gactggcaat caaactgtaa gtacggcaag ccagttcaaa ttaaagggtg cataccctca 900

atcgtgctgt gcaatccagg agaggggagc agttatataa gtttcctcaa caaagaggaa 960  
aatgcatcac taagagcgtg gactacacaaa aatgcaaaat tcatcactct tgaagccccc 1020  
ctctatcaaa gcacagcaca agattgc 1047

<210> 111  
<211> 1047  
<212> DNA  
<213> cabbage leaf curl virus

<220>  
<221> CDS  
<222> (1)..(1047)  
<223> CbLCV AL1 L145A mutation

<400> 111  
atg cca cga aac cct aaa tcg ttt cgt tta gca gcc cga aat ata ttc 48  
Met Pro Arg Asn Pro Lys Ser Phe Arg Leu Ala Ala Arg Asn Ile Phe  
1 5 10 15  
tta aca tat ccc cag tgc gac ata ccc aaa gat gaa gct ctt cag atg 96  
Leu Thr Tyr Pro Gln Cys Asp Ile Pro Lys Asp Glu Ala Leu Gln Met  
20 25 30  
ctt caa acc ctg tcg tgg tca gtc gtc aaa ccc aca tac atc aga gtc 144  
Leu Gln Thr Leu Ser Trp Ser Val Val Lys Pro Thr Tyr Ile Arg Val  
35 40 45  
gca aga gag gaa cat tca gac ggg ttc ccc cat tta cac tgt ctc atc 192  
Ala Arg Glu Glu His Ser Asp Gly Phe Pro His Leu His Cys Leu Ile  
50 55 60  
caa cta tca gga aag tcg aac atc aag gat gct aga ttt ttc gac atc 240  
Gln Leu Ser Gly Lys Ser Asn Ile Lys Asp Ala Arg Phe Phe Asp Ile  
65 70 75 80  
act cac ccc aga agg tct gcc aat ttt cac cca aac att cag gca gcc 288  
Thr His Pro Arg Arg Ser Ala Asn Phe His Pro Asn Ile Gln Ala Ala  
85 90 95  
aaa gac acc aat gcc gtc aag aat tac atc acc aaa gat ggt gat tat 336  
Lys Asp Thr Asn Ala Val Lys Asn Tyr Ile Thr Lys Asp Gly Asp Tyr  
100 105 110  
tgt gaa tcc ggg cag tac aag gtg tct ggg ggt aca aag gca aat aaa 384  
Cys Glu Ser Gly Gln Tyr Lys Val Ser Gly Gly Thr Lys Ala Asn Lys  
115 120 125  
gac gac gtc tac cac aac gcc gtc aat gcg gga tgt gtg gaa gag gcg 432  
Asp Asp Val Tyr His Asn Ala Val Asn Ala Gly Cys Val Glu Glu Ala  
130 135 140  
gcc gca att ata agg gct gga gat cca aag acg ttc att gtt agt tat 480

Ala Ala Ile Ile Arg Ala Gly Asp Pro Lys Thr Phe Ile Val Ser Tyr	
145 150 155 160	
cat aat gtt aga gct aac ata gag cga ctc ttt act aag gct ccg gaa	528
His Asn Val Arg Ala Asn Ile Glu Arg Leu Phe Thr Lys Ala Pro Glu	
165 170 175	
cca tgg gct cct ccg ttt caa ctc tcc tcc ttt act aac gtc ccg gac	576
Pro Trp Ala Pro Pro Phe Gln Leu Ser Ser Phe Thr Asn Val Pro Asp	
180 185 190	
gag atg agt tca tgg gca gat gac tat ttt ggt cgg agt gcc gct gcg	624
Glu Met Ser Ser Trp Ala Asp Tyr Phe Gly Arg Ser Ala Ala Ala	
195 200 205	
cgg gcg gaa aga cct att agt atc ata gtt gaa ggt gat tca cga acc	672
Arg Ala Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser Arg Thr	
210 215 220	
ggc aag acc atg tgg gcg cgt gct tta gga cca cat aat tat ttg agt	720
Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr Leu Ser	
225 230 235 240	
ggg cac ctc gac ttt aat tca aag gtc ttt tca aat aat gcg gag tat	768
Gly His Leu Asp Phe Asn Ser Lys Val Phe Ser Asn Asn Ala Glu Tyr	
245 250 255	
aac gtc att gat gac ata gct ccg cat tat cta aag cta aag cac tgg	816
Asn Val Ile Asp Asp Ile Ala Pro His Tyr Leu Lys Leu Lys His Trp	
260 265 270	
aaa gag ctt att ggg gcc caa agg gac tgg caa tca aac tgt aag tac	864
Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Ser Asn Cys Lys Tyr	
275 280 285	
ggc aag cca gtt caa att aaa ggt ggc ata ccc tca atc gtg ctg tgc	912
Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val Leu Cys	
290 295 300	
aat cca gga gag ggg agc agt tat ata agt ttc ctc aac aaa gag gaa	960
Asn Pro Gly Glu Gly Ser Ser Tyr Ile Ser Phe Leu Asn Lys Glu Glu	
305 310 315 320	
aat gca tca cta aga gcg tgg act acc aaa aat gca aaa ttc atc act	1008
Asn Ala Ser Leu Arg Ala Trp Thr Thr Lys Asn Ala Lys Phe Ile Thr	
325 330 335	
ctt gaa gcc ccc ctc tat caa agc aca gca caa gat tgc	1047
Leu Glu Ala Pro Leu Tyr Gln Ser Thr Ala Gln Asp Cys	
340 345	
<210> 112	
<211> 349	
<212> PRT	
<213> cabbage leaf curl virus	



<400> 112

Met Pro Arg Asn Pro Lys Ser Phe Arg Leu Ala Ala Arg Asn Ile Phe  
1 5 10 15

Leu Thr Tyr Pro Gln Cys Asp Ile Pro Lys Asp Glu Ala Leu Gln Met  
20 25 30

Leu Gln Thr Leu Ser Trp Ser Val Val Lys Pro Thr Tyr Ile Arg Val  
35 40 45

Ala Arg Glu Glu His Ser Asp Gly Phe Pro His Leu His Cys Leu Ile  
50 55 60

Gln Leu Ser Gly Lys Ser Asn Ile Lys Asp Ala Arg Phe Phe Asp Ile  
65 70 75 80

Thr His Pro Arg Arg Ser Ala Asn Phe His Pro Asn Ile Gln Ala Ala  
85 90 95

Lys Asp Thr Asn Ala Val Lys Asn Tyr Ile Thr Lys Asp Gly Asp Tyr  
100 105 110

Cys Glu Ser Gly Gln Tyr Lys Val Ser Gly Gly Thr Lys Ala Asn Lys  
115 120 125

Asp Asp Val Tyr His Asn Ala Val Asn Ala Gly Cys Val Glu Glu Ala  
130 135 140

Ala Ala Ile Ile Arg Ala Gly Asp Pro Lys Thr Phe Ile Val Ser Tyr  
145 150 155 160

His Asn Val Arg Ala Asn Ile Glu Arg Leu Phe Thr Lys Ala Pro Glu  
165 170 175

Pro Trp Ala Pro Pro Phe Gln Leu Ser Ser Phe Thr Asn Val Pro Asp  
180 185 190

Glu Met Ser Ser Trp Ala Asp Asp Tyr Phe Gly Arg Ser Ala Ala Ala  
195 200 205

Arg Ala Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser Arg Thr  
210 215 220

Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr Leu Ser  
 225 230 235 240

Gly His Leu Asp Phe Asn Ser Lys Val Phe Ser Asn Asn Ala Glu Tyr  
 245 250 255

Asn Val Ile Asp Asp Ile Ala Pro His Tyr Leu Lys Leu Lys His Trp  
 260 265 270

Lys Glu Leu Ile Gly Ala Gln Arg Asp Trp Gln Ser Asn Cys Lys Tyr  
 275 280 285

Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val Leu Cys  
 290 295 300

Asn Pro Gly Glu Gly Ser Ser Tyr Ile Ser Phe Leu Asn Lys Glu Glu  
 305 310 315 320

Asn Ala Ser Leu Arg Ala Trp Thr Thr Lys Asn Ala Lys Phe Ile Thr  
 325 330 335

Leu Glu Ala Pro Leu Tyr Gln Ser Thr Ala Gln Asp Cys  
 340 345